

10 20 30 40
 * * * *
 ATG TCT GCA CTT CTG ATC CTA GCT CTT GTT GGA GCT GCA GTT GCT
 Met Ser Ala Leu Leu Ile Leu Ala Leu Val Gly Ala Ala Val Ala>
 _a_a_a_a_TRYPSIN SIGNAL SEQUENCE_a_a_a_a_>
 50 60 70 80 90
 * * * * *
 AGA GAC TGT GCA GAT GTA TAT CAA GCT GGT TTT AAT AAA AGT GGA
 Arg Asp Cys Ala Asp Val Tyr Gln Ala Gly Phe Asn Lys Ser Gly>
 _b_b_b_ANG1 FIBRINOGEN-LIKE DOMAIN_b_b_b_b_>
 100 110 120 130
 * * * * *
 ATC TAC ACT ATT TAT ATT AAT AAT ATG CCA GAA CCC AAA AAG GTG
 Ile Tyr Thr Ile Tyr Ile Asn Asn Met Pro Glu Pro Lys Lys Val>
 _b_b_b_ANG1 FIBRINOGEN-LIKE DOMAIN_b_b_b_b_>
 140 150 160 170 180
 * * * * *
 TTT TGC AAT ATG GAT GTC AAT GGG GGA GGT TGG ACT GTA ATA CAA
 Phe Cys Asn Met Asp Val Asn Gly Gly Gly Trp Thr Val Ile Gln>
 _b_b_b_ANG1 FIBRINOGEN-LIKE DOMAIN_b_b_b_b_>
 190 200 210 220
 * * * * *
 CAT CGT GAA GAT GGA AGT CTA GAT TTC CAA AGA GGC TGG AAG GAA
 His Arg Glu Asp Gly Ser Leu Asp Phe Gln Arg Gly Trp Lys Glu>
 _b_b_b_ANG1 FIBRINOGEN-LIKE DOMAIN_b_b_b_b_>
 230 240 250 260 270
 * * * * *
 TAT AAA ATG GGT TTT GGA AAT CCC TCC GGT GAA TAT TGG CTG GGG
 Tyr Lys Met Gly Phe Gly Asn Pro Ser Gly Glu Tyr Trp Leu Gly>
 _b_b_b_ANG1 FIBRINOGEN-LIKE DOMAIN_b_b_b_b_>
 280 290 300 310
 * * * * *
 AAT GAG TTT ATT TTT GCC ATT ACC AGT CAG AGG CAG TAC ATG CTA
 Asn Glu Phe Ile Phe Ala Ile Thr Ser Gln Arg Gln Tyr Met Leu>
 _b_b_b_ANG1 FIBRINOGEN-LIKE DOMAIN_b_b_b_b_>
 320 330 340 350 360
 * * * * *
 AGA ATT GAG TTA ATG GAC TGG GAA GGG AAC CGA GCC TAT TCA CAG
 Arg Ile Glu Leu Met Asp Trp Glu Gly Asn Arg Ala Tyr Ser Gln>
 _b_b_b_ANG1 FIBRINOGEN-LIKE DOMAIN_b_b_b_b_>
 370 380 390 400
 * * * * *
 TAT GAC AGA TTC CAC ATA GGA AAT GAA AAG CAA AAC TAT AGG TTG
 Tyr Asp Arg Phe His Ile Gly Asn Glu Lys Gln Asn Tyr Arg Leu>
 _b_b_b_ANG1 FIBRINOGEN-LIKE DOMAIN_b_b_b_b_>
 410 420 430 440 450
 * * * * *
 TAT TTA AAA GGT CAC ACT GGG ACA GCA GGA AAA CAG AGC AGC CTG
 Tyr Leu Lys Gly His Thr Gly Thr Ala Gly Lys Gln Ser Ser Leu>
 _b_b_b_ANG1 FIBRINOGEN-LIKE DOMAIN_b_b_b_b_>

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*      *      *      *      *      *      *      *
460      470      480      490
ATC TTA CAC GGT GCT GAT TTC AGC ACT AAA GAT GCT GAT AAT GAC
Ile Leu His Gly Ala Asp Phe Ser Thr Lys Asp Ala Asp Asn Asp>
__b__b__b__ANG1 FIBRINOGEN-LIKE DOMAIN_b__b__b__b__>

500      510      520      530      540
*      *      *      *      *      *      *      *
AAC TGT ATG TGC AAA TGT GCC CTC ATG TTA ACA GGA GGA TGG TGG
Asn Cys Met Cys Lys Cys Ala Leu Met Leu Thr Gly Gly Trp Trp>
__b__b__b__ANG1 FIBRINOGEN-LIKE DOMAIN_b__b__b__b__>

550      560      570      580
*      *      *      *      *      *      *      *
TTT GAT GCT TGT GGC CCC TCC AAT CTA AAT GGA ATG TTC TAT ACT
Phe Asp Ala Cys Gly Pro Ser Asn Leu Asn Gly Met Phe Tyr Thr>
__b__b__b__ANG1 FIBRINOGEN-LIKE DOMAIN_b__b__b__b__>

590      600      610      620      630
*      *      *      *      *      *      *      *
GCG GGA CAA AAC CAT GGA AAA CTG AAT GGG ATA AAG TGG CAC TAC
Ala Gly Gln Asn His Gly Lys Leu Asn Gly Ile Lys Trp His Tyr>
__b__b__b__ANG1 FIBRINOGEN-LIKE DOMAIN_b__b__b__b__>

640      650      660      670
*      *      *      *      *      *      *      *
TTC AAA GGG CCC AGT TAC TCC TTA CGT TCC ACA ACT ATG ATG ATT
Phe Lys Gly Pro Ser Tyr Ser Leu Arg Ser Thr Thr Met Met Ile>
__b__b__b__ANG1 FIBRINOGEN-LIKE DOMAIN_b__b__b__b__>

680      690      700      710      720
*      *      *      *      *      *      *      *
CGA CCT TTA GAT TTT GGC CCC GCG CCT TTT AGA GAC TGT GCA GAT
Arg Pro Leu Asp Phe>
__ANG1 FIBRINO__>
      Gly Pro Ala Pro>
      __GPAP BRI__>
      Phe Arg Asp Cys Ala Asp>
      __ANG1 FIBRINOGEN-__>

730      740      750      760
*      *      *      *      *      *      *      *
GTA TAT CAA GCT GGT TTT AAT AAA AGT GGA ATC TAC ACT ATT TAT
Val Tyr Gln Ala Gly Phe Asn Lys Ser Gly Ile Tyr Thr Ile Tyr>
__d__d__d__ANG1 FIBRINOGEN-LIKE DOMAIN_d__d__d__d__>

770      780      790      800      810
*      *      *      *      *      *      *      *
ATT AAT AAT ATG CCA GAA CCC AAA AAG GTG TTT TGC AAT ATG GAT
Ile Asn Asn Met Pro Glu Pro Lys Lys Val Phe Cys Asn Met Asp>
__d__d__d__ANG1 FIBRINOGEN-LIKE DOMAIN_d__d__d__d__>

820      830      840      850
*      *      *      *      *      *      *      *
GTC AAT GGG GGA GGT TGG ACT GTA ATA CAA CAT CGT GAA GAT GGA
Val Asn Gly Gly Gly Trp Thr Val Ile Gln His Arg Glu Asp Gly>
__d__d__d__ANG1 FIBRINOGEN-LIKE DOMAIN_d__d__d__d__>

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      860      870      880      890      900
      *        *        *        *        *
AGT CTA GAT TTC CAA AGA GGC TGG AAG GAA TAT AAA ATG GGT TTT
Ser Leu Asp Phe Gln Arg Gly Trp Lys Glu Tyr Lys Met Gly Phe>
_d_d_d_ANG1 FIBRINOGEN-LIKE DOMAIN_d_d_d_d_>

      910      920      930      940
      *        *        *        *        *
GGA AAT CCC TCC GGT GAA TAT TGG CTG GGG AAT GAG TTT ATT TTT
Gly Asn Pro Ser Gly Glu Tyr Trp Leu Gly Asn Glu Phe Ile Phe>
_d_d_d_ANG1 FIBRINOGEN-LIKE DOMAIN_d_d_d_d_>

      950      960      970      980      990
      *        *        *        *        *
GCC ATT ACC AGT CAG AGG CAG TAC ATG CTA AGA ATT GAG TTA ATG
Ala Ile Thr Ser Gln Arg Gln Tyr Met Leu Arg Ile Glu Leu Met>
_d_d_d_ANG1 FIBRINOGEN-LIKE DOMAIN_d_d_d_d_>

      1000     1010     1020     1030
      *        *        *        *        *
GAC TGG GAA GGG AAC CGA GCC TAT TCA CAG TAT GAC AGA TTC CAC
Asp Trp Glu Gly Asn Arg Ala Tyr Ser Gln Tyr Asp Arg Phe His>
_d_d_d_ANG1 FIBRINOGEN-LIKE DOMAIN_d_d_d_d_>

      1040     1050     1060     1070     1080
      *        *        *        *        *
ATA GGA AAT GAA AAG CAA AAC TAT AGG TTG TAT TTA AAA GGT CAC
Ile Gly Asn Glu Lys Gln Asn Tyr Arg Leu Tyr Leu Lys Gly His>
_d_d_d_ANG1 FIBRINOGEN-LIKE DOMAIN_d_d_d_d_>

      1090     1100     1110     1120
      *        *        *        *        *
ACT GGG ACA GCA GGA AAA CAG AGC AGC CTG ATC TTA CAC GGT GCT
Thr Gly Thr Ala Gly Lys Gln Ser Ser Leu Ile Leu His Gly Ala>
_d_d_d_ANG1 FIBRINOGEN-LIKE DOMAIN_d_d_d_d_>

      1130     1140     1150     1160     1170
      *        *        *        *        *
GAT TTC AGC ACT AAA GAT GCT GAT AAT GAC AAC TGT ATG TGC AAA
Asp Phe Ser Thr Lys Asp Ala Asp Asn Asp Asn Cys Met Cys Lys>
_d_d_d_ANG1 FIBRINOGEN-LIKE DOMAIN_d_d_d_d_>

      1180     1190     1200     1210
      *        *        *        *        *
TGT GCC CTC ATG TTA ACA GGA GGA TGG TGG TTT GAT GCT TGT GGC
Cys Ala Leu Met Leu Thr Gly Gly Trp Trp Phe Asp Ala Cys Gly>
_d_d_d_ANG1 FIBRINOGEN-LIKE DOMAIN_d_d_d_d_>

      1220     1230     1240     1250     1260
      *        *        *        *        *
CCC TTC AAT CTA AAT GGA ATG TTC TAT ACT GCG GGA CAA AAC CAT
Pro Ser Asn Leu Asn Gly Met Phe Tyr Thr Ala Gly Gln Asn His>
_d_d_d_ANG1 FIBRINOGEN-LIKE DOMAIN_d_d_d_d_>

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4/42
Figure 1D

1270 1280 1290 1300

* * * * *

GGA AAA CTG AAT GGG ATA AAG TGG CAC TAC TTC AAA GGG CCC AGT
Gly Lys Leu Asn Gly Ile Lys Trp His Tyr Phe Lys Gly Pro Ser>
_d_d_d_ANG1 FIBRINOGEN-LIKE DOMAIN_d_d_d_d_>

1310 1320 1330 1340 1350

* * * * *

TAC TCC TTA CGT TCC ACA ACT ATG ATG ATT CGA CCT TTA GAT TTT
Tyr Ser Leu Arg Ser Thr Thr Met Met Ile Arg Pro Leu Asp Phe>
_d_d_d_ANG1 FIBRINOGEN-LIKE DOMAIN_d_d_d_d_>

1360 1370 1380 1390

* * * * *

GGA CCG GGC GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA
Gly Pro Gly>
_e_e_>
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro>
_f_f_f_FC TAG [SPLIT]_f_f_f_f_>

1400 1410 1420 1430 1440

* * * * *

CCG TGC CCA GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC
Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu>
_f_f_f_f_f_FC TAG [SPLIT]_f_f_f_f_f_>

1450 1460 1470 1480

* * * * *

TTC CCC CCA AAA CCC AAG GAC ACC CTC ATG ATC TCC CGG ACC CCT
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro>
_f_f_f_f_f_FC TAG [SPLIT]_f_f_f_f_f_>

1490 1500 1510 1520 1530

* * * * *

GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC GAA GAC CCT GAG
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu>
_f_f_f_f_f_FC TAG [SPLIT]_f_f_f_f_f_>

1540 1550 1560 1570

* * * * *

GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT GCC
Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala>
_f_f_f_f_f_FC TAG [SPLIT]_f_f_f_f_f_>

1580 1590 1600 1610 1620

* * * * *

AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG
Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val>
_f_f_f_f_f_FC TAG [SPLIT]_f_f_f_f_f_>

1630 1640 1650 1660

* * * * *

GTC AGC GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys>
_f_f_f_f_f_FC TAG [SPLIT]_f_f_f_f_f_>

1670	1680	1690	1700	1710
* * * * * GAG TAC AAG TGC AAG GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile> _f_f_f_f_f_FC TAG [SPLIT]_f_f_f_f_f_>				
1720	1730	1740	1750	
* * * * * GAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC CGA GAA CCA CAG Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln> _f_f_f_f_f_FC TAG [SPLIT]_f_f_f_f_f_>				
1760	1770	1780	1790	1800
* * * * * GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG ACC AAG AAC CAG Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln> _f_f_f_f_f_FC TAG [SPLIT]_f_f_f_f_f_>				
1810	1820	1830	1840	
* * * * * GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC ATC Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile> _f_f_f_f_f_FC TAG [SPLIT]_f_f_f_f_f_>				
1850	1860	1870	1880	1890
* * * * * GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys> _f_f_f_f_f_FC TAG [SPLIT]_f_f_f_f_f_>				
1900	1910	1920	1930	
* * * * * ACC ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr> _f_f_f_f_f_FC TAG [SPLIT]_f_f_f_f_f_>				
1940	1950	1960	1970	1980
* * * * * AGC AAG CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val> _f_f_f_f_f_FC TAG [SPLIT]_f_f_f_f_f_>				
1990	2000	2010	2020	
* * * * * TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC ACG Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr> _f_f_f_f_f_FC TAG [SPLIT]_f_f_f_f_f_>				
2030	2040	2050		
* * * * * CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA TGA Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys >>> _f_f_f_f_f_FC TAG [SPLIT]_f_f_f_f_f_>				

Figure 2A

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      10      20      30      40
*      *      *      *      *
ATG TCT GCA CTT CTG ATC CTA GCT CTT GTT GGA GCT GCA GTT GCT
Met Ser Ala Leu Leu Ile Leu Ala Leu Val Gly Ala Ala Val Ala>
_a_a_a_a_TRYPSIN SIGNAL SEQUENCE_a_a_a_a_>

      50      60      70      80      90
*      *      *      *      *
AGA GAC TGT GCT GAA GTA TTC AAA TCA GGA CAC ACC ACA AAT GGC
Arg Asp Cys Ala Glu Val Phe Lys Ser Gly His Thr Thr Asn Gly>
_b_b_b_ANG2 FIBRINOGEN-LIKE DOMAIN #1_b_b_b_>

      100      110      120      130
*      *      *      *      *
ATC TAC ACG TTA ACA TTC CCT AAT TCT ACA GAA GAG ATC AAG GCC
Ile Tyr Thr Leu Thr Phe Pro Asn Ser Thr Glu Glu Ile Lys Ala>
_b_b_b_ANG2 FIBRINOGEN-LIKE DOMAIN #1_b_b_b_>

      140      150      160      170      180
*      *      *      *      *
TAC TGT GAC ATG GAA GCT GGA GGA GGC GGG TGG ACA ATT ATT CAG
Tyr Cys Asp Met Glu Ala Gly Gly Gly Gly Trp Thr Ile Ile Gln>
_b_b_b_ANG2 FIBRINOGEN-LIKE DOMAIN #1_b_b_b_>

      190      200      210      220
*      *      *      *      *
CGA CGT GAG GAT GGC AGC GTT GAT TTT CAG AGG ACT TGG AAA GAA
Arg Arg Glu Asp Gly Ser Val Asp Phe Gln Arg Thr Trp Lys Glu>
_b_b_b_ANG2 FIBRINOGEN-LIKE DOMAIN #1_b_b_b_>

      230      240      250      260      270
*      *      *      *      *
TAT AAA GTG GGA TTT GGT AAC CCT TCA GGA GAA TAT TGG CTG GGA
Tyr Lys Val Gly Phe Gly Asn Pro Ser Gly Glu Tyr Trp Leu Gly>
_b_b_b_ANG2 FIBRINOGEN-LIKE DOMAIN #1_b_b_b_>

      280      290      300      310
*      *      *      *      *
AAT GAG TTT GTT TCG CAA CTG ACT AAT CAG CAA CGC TAT GTG CTT
Asn Glu Phe Val Ser Gln Leu Thr Asn Gln Gln Arg Tyr Val Leu>
_b_b_b_ANG2 FIBRINOGEN-LIKE DOMAIN #1_b_b_b_>

      320      330      340      350      360
*      *      *      *      *
AAA ATA CAC CTT AAA GAC TGG GAA GGG AAT GAG GCT TAC TCA TTG
Lys Ile His Leu Lys Asp Trp Glu Gly Asn Glu Ala Tyr Ser Leu>
_b_b_b_ANG2 FIBRINOGEN-LIKE DOMAIN #1_b_b_b_>

      370      380      390      400
*      *      *      *      *
TAT GAA CAT TTC TAT CTC TCA AGT GAA GAA CTC AAT TAT AGG ATT
Tyr Glu His Phe Tyr Leu Ser Ser Glu Glu Leu Asn Tyr Arg Ile>
_b_b_b_ANG2 FIBRINOGEN-LIKE DOMAIN #1_b_b_b_>

      410      420      430      440      450
*      *      *      *      *
CAC CTT AAA GGA CTT ACA GGG ACA GCC GGC AAA ATA AGC AGC ATC
His Leu Lys Gly Leu Thr Gly Thr Ala Gly Lys Ile Ser Ser Ile>
_b_b_b_ANG2 FIBRINOGEN-LIKE DOMAIN #1_b_b_b_>

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7/42
Figure 2B

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      460      470      480      490
      *      *      *      *
AGC CAA CCA GGA AAT GAT TTT AGC ACA AAG GAT GGA GAC AAC GAC
Ser Gln Pro Gly Asn Asp Phe Ser Thr Lys Asp Gly Asp Asn Asp>
__b__b__b__ANG2 FIBRINOGEN-LIKE DOMAIN #1__b__b__b__>

      500      510      520      530      540
      *      *      *      *      *
AAA TGT ATT TGC AAA TGT TCA CAA ATG CTA ACA GGA GGC TGG TGG
Lys Cys Ile Cys Lys Cys Ser Gln Met Leu Thr Gly Gly Trp Trp>
__b__b__b__ANG2 FIBRINOGEN-LIKE DOMAIN #1__b__b__b__>

      550      560      570      580
      *      *      *      *
TTT GAT GCA TGT GGT CCT TCC AAC TTG AAC GGA ATG TAC TAT CCA
Phe Asp Ala Cys Gly Pro Ser Asn Leu Asn Gly Met Tyr Tyr Pro>
__b__b__b__ANG2 FIBRINOGEN-LIKE DOMAIN #1__b__b__b__>

      590      600      610      620      630
      *      *      *      *      *
CAG AGG CAG AAC ACA AAT AAG TTC AAC GGC ATT AAA TGG TAC TAC
Gln Arg Gln Asn Thr Asn Lys Phe Asn Gly Ile Lys Trp Tyr Tyr>
__b__b__b__ANG2 FIBRINOGEN-LIKE DOMAIN #1__b__b__b__>

      640      650      660      670
      *      *      *      *
TGG AAA GGC TCA GGC TAT TCG CTC AAG GCC ACA ACC ATG ATG ATC
Trp Lys Gly Ser Gly Tyr Ser Leu Lys Ala Thr Thr Met Met Ile>
__b__b__b__ANG2 FIBRINOGEN-LIKE DOMAIN #1__b__b__b__>

      680      690      700      710      720
      *      *      *      *      *
CGA CCA GCA GAT TTC GGG GGC CCC GCG CCT TTC AGA GAC TGT GCT
Arg Pro Ala Asp Phe>
__ANG2 FIBRINO__>
      Gly Gly Pro Ala Pro>
      __GGPAP BRIDGE__>
      Phe Arg Asp Cys Ala>
      __ANG2 FIBRINO__>

      730      740      750      760
      *      *      *      *
GAA GTA TTC AAA TCA GGA CAC ACC ACA AAT GGC ATC TAC ACG TTA
Glu Val Phe Lys Ser Gly His Thr Thr Asn Gly Ile Tyr Thr Leu>
__d__d__d__ANG2 FIBRINOGEN-LIKE DOMAIN#2__d__d__d__>

      770      780      790      800      810
      *      *      *      *      *
ACA TTC CCT AAT TCT ACA GAA GAG ATC AAG GCC TAC TGT GAC ATG
Thr Phe Pro Asn Ser Thr Glu Glu Ile Lys Ala Tyr Cys Asp Met>
__d__d__d__ANG2 FIBRINOGEN-LIKE DOMAIN#2__d__d__d__>

      820      830      840      850
      *      *      *      *
GAA GCT GGA GGA GGC GGG TGG ACA ATT ATT CAG CGA CGT GAG GAT
Glu Ala Gly Gly Gly Gly Trp Thr Ile Ile Gln Arg Glu Asp>
__d__d__d__ANG2 FIBRINOGEN-LIKE DOMAIN#2__d__d__d__>

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05065537-100101

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      860      870      880      890      900
      *        *        *        *        *
GGC AGC GTT GAT TTT CAG AGG ACT TGG AAA GAA TAT AAA GTG GGA
Gly Ser Val Asp Phe Gln Arg Thr Trp Lys Glu Tyr Lys Val Gly>
_d_d_d_ANG2 FIBRINOGEN-LIKE DOMAIN#2_d_d_d_>

      910      920      930      940
      *        *        *        *        *
TTT GGT AAC CCT TCA GGA GAA TAT TGG CTG GGA AAT GAG TTT GTT
Phe Gly Asn Pro Ser Gly Glu Tyr Trp Leu Gly Asn Glu Phe Val>
_d_d_d_ANG2 FIBRINOGEN-LIKE DOMAIN#2_d_d_d_>

      950      960      970      980      990
      *        *        *        *        *
TCG CAA CTG ACT AAT CAG CAA CGC TAT GTG CTT AAA ATA CAC CTT
Ser Gln Leu Thr Asn Gln Gln Arg Tyr Val Leu Lys Ile His Leu>
_d_d_d_ANG2 FIBRINOGEN-LIKE DOMAIN#2_d_d_d_>

      1000     1010     1020     1030
      *        *        *        *        *
AAA GAC TGG GAA GGG AAT GAG GCT TAC TCA TTG TAT GAA CAT TTC
Lys Asp Trp Glu Gly Asn Glu Ala Tyr Ser Leu Tyr Glu His Phe>
_d_d_d_ANG2 FIBRINOGEN-LIKE DOMAIN#2_d_d_d_>

      1040     1050     1060     1070     1080
      *        *        *        *        *
TAT CTC TCA AGT GAA GAA CTC AAT TAT AGG ATT CAC CTT AAA GGA
Tyr Leu Ser Ser Glu Glu Leu Asn Tyr Arg Ile His Leu Lys Gly>
_d_d_d_ANG2 FIBRINOGEN-LIKE DOMAIN#2_d_d_d_>

      1090     1100     1110     1120
      *        *        *        *        *
CTT ACA GGG ACA GCC GGC AAA ATA AGC AGC ATC AGC CAA CCA GGA
Leu Thr Gly Thr Ala Gly Lys Ile Ser Ser Ile Ser Gln Pro Gly>
_d_d_d_ANG2 FIBRINOGEN-LIKE DOMAIN#2_d_d_d_>

      1130     1140     1150     1160     1170
      *        *        *        *        *
AAT GAT TTT AGC ACA AAG GAT GGA GAC AAC GAC AAA TGT ATT TGC
Asn Asp Phe Ser Thr Lys Asp Gly Asp Asn Asp Lys Cys Ile Cys>
_d_d_d_ANG2 FIBRINOGEN-LIKE DOMAIN#2_d_d_d_>

      1180     1190     1200     1210
      *        *        *        *        *
AAA TGT TCA CAA ATG CTA ACA GGA GGC TGG TTT GAT GCA TGT
Lys Cys Ser Gln Met Leu Thr Gly Gly Trp Trp Phe Asp Ala Cys>
_d_d_d_ANG2 FIBRINOGEN-LIKE DOMAIN#2_d_d_d_>

      1220     1230     1240     1250     1260
      *        *        *        *        *
GGT CCT TCC AAC TTG AAC GGA ATG TAC TAT CCA CAG AGG CAG AAC
Gly Pro Ser Asn Leu Asn Gly Met Tyr Tyr Pro Gln Arg Gln Asn>
_d_d_d_ANG2 FIBRINOGEN-LIKE DOMAIN#2_d_d_d_>

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9/42
Figure 2D

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      1270      1280      1290      1300
      *      *      *      *      *
ACA AAT AAG TTC AAC GGC ATT AAA TGG TAC TAC TGG AAA GGC TCA
Thr Asn Lys Phe Asn Gly Ile Lys Trp Tyr Tyr Trp Lys Gly Ser>
_d_d_d_d_ANG2 FIBRINOGEN-LIKE DOMAIN#2_d_d_d_d_>

      1310      1320      1330      1340      1350
      *      *      *      *      *
GGC TAT TCG CTC AAG GCC ACA ACC ATG ATG ATC CGA CCA GCA GAT
Gly Tyr Ser Leu Lys Ala Thr Thr Met Met Ile Arg Pro Ala Asp>
_d_d_d_d_ANG2 FIBRINOGEN-LIKE DOMAIN#2_d_d_d_d_>

      1360      1370      1380      1390
      *      *      *      *      *
TTC GGA CCG GGC GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC
Phe>
____
      Gly Pro Gly>
      _e_e_>
              Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys>
              _f_f_f_f_f_FC TAG_f_f_f_f_f_>

      1400      1410      1420      1430      1440
      *      *      *      *      *
CCA CCG TGC CCA GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC TTC
Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe>
_f_f_f_f_f_f_f_FC TAG_f_f_f_f_f_f_f_f_>

      1450      1460      1470      1480
      *      *      *      *      *
CTC TTC CCC CCA AAA CCC AAG GAC ACC CTC ATG ATC TCC CGG ACC
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr>
_f_f_f_f_f_f_f_FC TAG_f_f_f_f_f_f_f_f_>

      1490      1500      1510      1520      1530
      *      *      *      *      *
CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC GAA GAC CCT
Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro>
_f_f_f_f_f_f_f_FC TAG_f_f_f_f_f_f_f_f_>

      1540      1550      1560      1570
      *      *      *      *      *
GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT
Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn>
_f_f_f_f_f_f_f_FC TAG_f_f_f_f_f_f_f_f_>

      1580      1590      1600      1610      1620
      *      *      *      *      *
GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg>
_f_f_f_f_f_f_f_FC TAG_f_f_f_f_f_f_f_f_>

      1630      1640      1650      1660
      *      *      *      *      *
GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly>
_f_f_f_f_f_f_f_FC TAG_f_f_f_f_f_f_f_f_>

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1670				1680				1690				1700				1710			
AAG	GAG	TAC	AAG	TGC	AAG	GTC	TCC	AAC	AAA	GCC	CTC	CCA	GCC	CCC					
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	>				
f				_f_				_f_				_f_				_f_			
FC				TAG				_f_				_f_				_f_			
1720				1730				1740				1750							
ATC	GAG	AAA	ACC	ATC	TCC	AAA	GCC	AAA	GGG	CAG	CCC	CGA	GAA	CCA					
Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	>				
f				_f_				_f_				_f_				_f_			
FC				TAG				_f_				_f_				_f_			
1760				1770				1780				1790				1800			
CAG	GTG	TAC	ACC	CTG	CCC	CCA	TCC	CGG	GAT	GAG	CTG	ACC	AAG	AAC					
Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	>				
f				_f_				_f_				_f_				_f_			
FC				TAG				_f_				_f_				_f_			
1810				1820				1830				1840							
CAG	GTC	AGC	CTG	ACC	TGC	CTG	GTC	AAA	GGC	TTC	TAT	CCC	AGC	GAC					
Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	>				
f				_f_				_f_				_f_				_f_			
FC				TAG				_f_				_f_				_f_			
1850				1860				1870				1880				1890			
ATC	GCC	GTG	GAG	TGG	GAG	AGC	AAT	GGG	CAG	CCG	GAG	AAC	AAC	TAC					
Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	>				
f				_f_				_f_				_f_				_f_			
FC				TAG				_f_				_f_				_f_			
1900				1910				1920				1930							
AAG	ACC	ACG	CCT	CCC	GTG	CTG	GAC	TCC	GAC	GGC	TCC	TTC	TTC	CTC					
Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	>				
f				_f_				_f_				_f_				_f_			
FC				TAG				_f_				_f_				_f_			
1940				1950				1960				1970				1980			
TAC	AGC	AAG	CTC	ACC	GTG	GAC	AAG	AGC	AGG	TGG	CAG	CAG	GGG	AAC					
Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	>				
f				_f_				_f_				_f_				_f_			
FC				TAG				_f_				_f_				_f_			
1990				2000				2010				2020							
GTC	TTC	TCA	TGC	TCC	GTG	ATG	CAT	GAG	GCT	CTG	CAC	AAC	CAC	TAC					
Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	>				
f				_f_				_f_				_f_				_f_			
FC				TAG				_f_				_f_				_f_			
2030				2040				2050				2060							
ACG	CAG	AAG	AGC	CTC	TCC	CTG	TCT	CCG	GGT	AAA	TGA								
Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys	***	>							
f				_f_				_f_				_f_				_f_			
FC				TAG				_f_				_f_				_f_			

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      10      20      30      40
*      *      *      *      *
ATG TCT GCA CTT CTG ATC CTA GCT CTT GTT GGA GCT GCA GTT GCT
Met Ser Ala Leu Leu Ile Leu Ala Leu Val Gly Ala Ala Val Ala>
_a_a_a_a_TRYPSIN SIGNAL SEQUENCE_a_a_a_a>

      50      60      70      80      90
*      *      *      *      *
AGA GAC TGT GCA GAT GTA TAT CAA GCT GGT TTT AAT AAA AGT GGA
Arg Asp Cys Ala Asp Val Tyr Gln Ala Gly Phe Asn Lys Ser Gly>
_b_b_b_b_ANG1 FIBRINOGEN-LIKE DOMAIN_b_b_b_b>

      100     110     120     130
*      *      *      *      *
ATC TAC ACT ATT TAT ATT AAT AAT ATG CCA GAA CCC AAA AAG GTG
Ile Tyr Thr Ile Tyr Ile Asn Asn Met Pro Glu Pro Lys Lys Val>
_b_b_b_b_ANG1 FIBRINOGEN-LIKE DOMAIN_b_b_b_b>

      140     150     160     170     180
*      *      *      *      *
TTT TGC AAT ATG GAT GTC AAT GGG GGA GGT TGG ACT GTA ATA CAA
Phe Cys Asn Met Asp Val Asn Gly Gly Gly Trp Thr Val Ile Gln>
_b_b_b_b_ANG1 FIBRINOGEN-LIKE DOMAIN_b_b_b_b>

      190     200     210     220
*      *      *      *      *
CAT CGT GAA GAT GGA AGT CTA GAT TTC CAA AGA GGC TGG AAG GAA
His Arg Glu Asp Gly Ser Leu Asp Phe Gln Arg Gly Trp Lys Glu>
_b_b_b_b_ANG1 FIBRINOGEN-LIKE DOMAIN_b_b_b_b>

      230     240     250     260     270
*      *      *      *      *
TAT AAA ATG GGT TTT GGA AAT CCC TCC GGT GAA TAT TGG CTG GGG
Tyr Lys Met Gly Phe Gly Asn Pro Ser Gly Glu Tyr Trp Leu Gly>
_b_b_b_b_ANG1 FIBRINOGEN-LIKE DOMAIN_b_b_b_b>

      280     290     300     310
*      *      *      *      *
AAT GAG TTT ATT TTT GCC ATT ACC AGT CAG AGG CAG TAC ATG CTA
Asn Glu Phe Ile Phe Ala Ile Thr Ser Gln Arg Gln Tyr Met Leu>
_b_b_b_b_ANG1 FIBRINOGEN-LIKE DOMAIN_b_b_b_b>

      320     330     340     350     360
*      *      *      *      *
AGA ATT GAG TTA ATG GAC TGG GAA GGG AAC CGA GCC TAT TCA CAG
Arg Ile Glu Leu Met Asp Trp Glu Gly Asn Arg Ala Tyr Ser Gln>
_b_b_b_b_ANG1 FIBRINOGEN-LIKE DOMAIN_b_b_b_b>

      370     380     390     400
*      *      *      *      *
TAT GAC AGA TTC CAC ATA GGA AAT GAA AAG CAA AAC TAT AGG TTG
Tyr Asp Arg Phe His Ile Gly Asn Glu Lys Gln Asn Tyr Arg Leu>
_b_b_b_b_ANG1 FIBRINOGEN-LIKE DOMAIN_b_b_b_b>

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410          420          430          440          450
*           *           *           *           *
TAT TTA AAA GGT CAC ACT GGG ACA GCA GGA AAA CAG AGC AGC CTG
Tyr Leu Lys Gly His Thr Gly Thr Ala Gly Lys Gln Ser Ser Leu>
__b__b__b__ANG1 FIBRINOGEN-LIKE DOMAIN__b__b__b__b__>

          460          470          480          490
*           *           *           *           *
ATC TTA CAC GGT GCT GAT TTC AGC ACT AAA GAT GCT GAT AAT GAC
Ile Leu His Gly Ala Asp Phe Ser Thr Lys Asp Ala Asp Asn Asp>
__b__b__b__ANG1 FIBRINOGEN-LIKE DOMAIN__b__b__b__b__>

          500          510          520          530          540
*           *           *           *           *
AAC TGT ATG TGC AAA TGT GCC CTC ATG TTA ACA GGA GGA TGG TGG
Asn Cys Met Cys Lys Cys Ala Leu Met Leu Thr Gly Gly Trp Trp>
__b__b__b__ANG1 FIBRINOGEN-LIKE DOMAIN__b__b__b__b__>

          550          560          570          580
*           *           *           *           *
TTT GAT GCT TGT GGC CCC TCC AAT CTA AAT GGA ATG TTC TAT ACT
Phe Asp Ala Cys Gly Pro Ser Asn Leu Asn Gly Met Phe Tyr Thr>
__b__b__b__ANG1 FIBRINOGEN-LIKE DOMAIN__b__b__b__b__>

          590          600          610          620          630
*           *           *           *           *
CGC GGA CAA AAC CAT GGA AAA CTG AAT GGG ATA AAG TGG CAC TAC
Ala Gly Gln Asn His Gly Lys Leu Asn Gly Ile Lys Trp His Tyr>
__b__b__b__ANG1 FIBRINOGEN-LIKE DOMAIN__b__b__b__b__>

          640          650          660          670
*           *           *           *           *
TTC AAA GGG CCA AGT TAC TCC TTA CGT TCC ACA ACT ATG ATG ATT
Phe Lys Gly Pro Ser Tyr Ser Leu Arg Ser Thr Thr Met Met Ile>
__b__b__b__ANG1 FIBRINOGEN-LIKE DOMAIN__b__b__b__b__>

          680          690          700          710          720
*           *           *           *           *
CGA CCT TTA GAT TTT GGC CCG GGC GAG CCC AAA TCT TGT GAC AAA
Arg Pro Leu Asp Phe>
__ANG1 FIBRINO__>
      Gly Pro Gly>
      __c__c__>
      Glu Pro Lys Ser Cys Asp Lys>
      __d__d__FC TAG__d__d__>

          730          740          750          760
*           *           *           *           *
ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT GAA CTC CTG GGG GGA
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly>
__d__d__d__d__d__d__FC TAG__d__d__d__d__d__d__>

          770          780          790          800          810
*           *           *           *           *
CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC CTC ATG
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met>
__d__d__d__d__d__d__FC TAG__d__d__d__d__d__d__>

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820 830 840 850

ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser>
_d_d_d_d_d_d_d_FC TAG_d_d_d_d_d_d_d_>

860 870 880 890 900

CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val>
_d_d_d_d_d_d_d_FC TAG_d_d_d_d_d_d_d_>

910 920 930 940

GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn>
_d_d_d_d_d_d_d_FC TAG_d_d_d_d_d_d_d_>

950 960 970 980 990

AGC ACG TAC CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG GAC
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp>
_d_d_d_d_d_d_d_FC TAG_d_d_d_d_d_d_d_>

1000 1010 1020 1030

TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GCC
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala>
_d_d_d_d_d_d_d_FC TAG_d_d_d_d_d_d_d_>

1040 1050 1060 1070 1080

CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA GGG CAG
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln>
_d_d_d_d_d_d_d_FC TAG_d_d_d_d_d_d_d_>

1090 1100 1110 1120

CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu>
_d_d_d_d_d_d_d_FC TAG_d_d_d_d_d_d_d_>

1130 1140 1150 1160 1170

CTG ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC
Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe>
_d_d_d_d_d_d_d_FC TAG_d_d_d_d_d_d_d_>

1180 1190 1200 1210

TAT CCC AGC GAC ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro>
_d_d_d_d_d_d_d_FC TAG_d_d_d_d_d_d_d_>

1220 1230 1240 1250 1260

GAG AAC AAC TAC AAG ACC ACG CCT CCC GTG CTG GAC TCC GAC GGC
Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly>
_d_d_d_d_d_d_d_FC TAG_d_d_d_d_d_d_d_>

14/42
Figure 3D

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1270      1280      1290      1300
*         *         *         *
TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG GAC AAG AGC AGG TGG
Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp>
_d_d_d_d_d_d_d_FC TAG_d_d_d_d_d_d_d_d>

1310      1320      1330      1340      1350
*         *         *         *         *
CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu>
_d_d_d_d_d_d_d_FC TAG_d_d_d_d_d_d_d_d>

1360      1370      1380      1390
*         *         *         *         *
CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys>
_d_d_d_d_d_d_d_FC TAG_d_d_d_d_d_d_d_d>

1400      1410      1420      1430      1440
*         *         *         *         *
GGC GGT GGC GGT TCT GGC GCG CCT TTT AGA GAC TGT GCA GAT GTA
Gly Gly Gly Gly Ser Gly Ala Pro>
_G4S LINKER/ASC BRIDGE (N____>
Phe Arg Asp Cys Ala Asp Val>
__ANG1 FIBRINOGEN-LIKE____>

1450      1460      1470      1480
*         *         *         *         *
TAT CAA GCT GGT TTT AAT AAA AGT GGA ATC TAC ACT ATT TAT ATT
Tyr Gln Ala Gly Phe Asn Lys Ser Gly Ile Tyr Thr Ile Tyr Ile>
__f__f__f__ANG1 FIBRINOGEN-LIKE DOMAIN_f__f__f__f__>

1490      1500      1510      1520      1530
*         *         *         *         *
AAT AAT ATG CCA GAA CCC AAA AAG GTG TTT TGC AAT ATG GAT GTC
Asn Asn Met Pro Glu Pro Lys Lys Val Phe Cys Asn Met Asp Val>
__f__f__f__ANG1 FIBRINOGEN-LIKE DOMAIN_f__f__f__f__>

1540      1550      1560      1570
*         *         *         *         *
AAT GGG GGA GGT TGG ACT GTA ATA CAA CAT CGT GAA GAT GGA AGT
Asn Gly Gly Gly Trp Thr Val Ile Gln His Arg Glu Asp Gly Ser>
__f__f__f__ANG1 FIBRINOGEN-LIKE DOMAIN_f__f__f__f__>

1580      1590      1600      1610      1620
*         *         *         *         *
CTA GAT TTC CAA AGA GGC TGG AAG GAA TAT AAA ATG GGT TTT GGA
Leu Asp Phe Gln Arg Gly Trp Lys Glu Tyr Lys Met Gly Phe Gly>
__f__f__f__ANG1 FIBRINOGEN-LIKE DOMAIN_f__f__f__f__>

1630      1640      1650      1660
*         *         *         *         *
AAT CCC TCC GGT GAA TAT TGG CTG GGG AAT GAG TTT ATT TTT GCC
Asn Pro Ser Gly Glu Tyr Trp Leu Gly Asn Glu Phe Ile Phe Ala>
__f__f__f__ANG1 FIBRINOGEN-LIKE DOMAIN_f__f__f__f__>

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16/42

Figure 4A

10 20 30 40
 * * * *
 ATG TCT GCA CTT CTG ATC CTA GCT CTT GTT GGA GCT GCA GTT GCT
 Met Ser Ala Leu Leu Ile Leu Ala Leu Val Gly Ala Ala Val Ala>
 _a_a_a_a_TRYPSIN SIGNAL SEQUENCE_a_a_a_a_>

50 60 70 80 90
 * * * * *
 AGA GAC TGT GCT GAA GTA TTC AAA TCA GGA CAC ACC ACA AAT GGC
 Arg Asp Cys Ala Glu Val Phe Lys Ser Gly His Thr Thr Asn Gly>
 _b_b_b_ANG2 FIBRINOGEN-LIKE DOMAIN_b_b_b_b_>

100 110 120 130
 * * * *
 ATC TAC ACG TTA ACA TTC CCT AAT TCT ACA GAA GAG ATC AAG GCC
 Ile Tyr Thr Leu Thr Phe Pro Asn Ser Thr Glu Glu Ile Lys Ala>
 _b_b_b_ANG2 FIBRINOGEN-LIKE DOMAIN_b_b_b_b_>

140 150 160 170 180
 * * * * *
 TAC TGT GAC ATG GAA GCT GGA GGC GGG TGG ACA ATT ATT CAG
 Tyr Cys Asp Met Glu Ala Gly Gly Gly Trp Thr Ile Ile Gln>
 _b_b_b_ANG2 FIBRINOGEN-LIKE DOMAIN_b_b_b_b_>

190 200 210 220
 * * * *
 CGA CGT GAG GAT GGC AGC GTT GAT TTT CAG AGG ACT TGG AAA GAA
 Arg Arg Glu Asp Gly Ser Val Asp Phe Gln Arg Thr Trp Lys Glu>
 _b_b_b_ANG2 FIBRINOGEN-LIKE DOMAIN_b_b_b_b_>

230 240 250 260 270
 * * * * *
 TAT AAA GTG GGA TTT GGT AAC CCT TCA GGA GAA TAT TGG CTG GGA
 Tyr Lys Val Gly Phe Gly Asn Pro Ser Gly Glu Tyr Trp Leu Gly>
 _b_b_b_ANG2 FIBRINOGEN-LIKE DOMAIN_b_b_b_b_>

280 290 300 310
 * * * *
 AAT GAG TTT GTT TCG CAA CTG ACT AAT CAG CAA CGC TAT GTG CTT
 Asn Glu Phe Val Ser Gln Leu Thr Asn Gln Gln Arg Tyr Val Leu>
 _b_b_b_ANG2 FIBRINOGEN-LIKE DOMAIN_b_b_b_b_>

320 330 340 350 360
 * * * * *
 AAA ATA CAC CTT AAA GAC TGG GAA GGG AAT GAG GCT TAC TCA TTG
 Lys Ile His Leu Lys Asp Trp Glu Gly Asn Glu Ala Tyr Ser Leu>
 _b_b_b_ANG2 FIBRINOGEN-LIKE DOMAIN_b_b_b_b_>

370 380 390 400
 * * * *
 TAT GAA CAT TTC TAT CTC TCA AGT GAA GAA CTC AAT TAT AGG ATT
 Tyr Glu His Phe Tyr Leu Ser Ser Glu Glu Leu Asn Tyr Arg Ile>
 _b_b_b_ANG2 FIBRINOGEN-LIKE DOMAIN_b_b_b_b_>

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410 420 430 440 450
* * * * *
CAC CTT AAA GGA CTT ACA GGG ACA GCC GGC AAA ATA AGC AGC ATC
His Leu Lys Gly Leu Thr Gly Thr Ala Gly Lys Ile Ser Ser Ile>
_b_b_b_ANG2 FIBRINOGEN-LIKE DOMAIN_b_b_b_b_>

 460 470 480 490
* * * * *
AGC CAA CCA GGA AAT GAT TTT AGC ACA AAG GAT GGA GAC AAC GAC
Ser Gln Pro Gly Asn Asp Phe Ser Thr Lys Asp Gly Asp Asn Asp>
_b_b_b_ANG2 FIBRINOGEN-LIKE DOMAIN_b_b_b_b_>

 500 510 520 530 540
* * * * *
AAA TGT ATT TGC AAA TGT TCA CAA ATG CTA ACA GGA GGC TGG TGG
Lys Cys Ile Cys Lys Cys Ser Gln Met Leu Thr Gly Gly Trp Trp>
_b_b_b_ANG2 FIBRINOGEN-LIKE DOMAIN_b_b_b_b_>

 550 560 570 580
* * * * *
TTT GAT GCA TGT GGT CCT TCC AAC TTG AAC GGA ATG TAC TAT CCA
Phe Asp Ala Cys Gly Pro Ser Asn Leu Asn Gly Met Tyr Tyr Pro>
_b_b_b_ANG2 FIBRINOGEN-LIKE DOMAIN_b_b_b_b_>

 590 600 610 620 630
* * * * *
CAG AGG CAG AAC ACA AAT AAG TTC AAC GGC ATT AAA TGG TAC TAC
Gln Arg Gln Asn Thr Asn Lys Phe Asn Gly Ile Lys Trp Tyr Tyr>
_b_b_b_ANG2 FIBRINOGEN-LIKE DOMAIN_b_b_b_b_>

 640 650 660 670
* * * * *
TGG AAA GGC TCA GGC TAT TCG CTC AAG GCC ACA ACC ATG ATG ATC
Trp Lys Gly Ser Gly Tyr Ser Leu Lys Ala Thr Thr Met Met Ile>
_b_b_b_ANG2 FIBRINOGEN-LIKE DOMAIN_b_b_b_b_>

 680 690 700 710 720
* * * * *
CGA CCA GCA GAT TTC GGG GGC CCG GGC GAG CCC AAA TCT TGT GAC
Arg Pro Ala Asp Phe>
ANG2 FIBRINO>
 Gly Gly Pro Gly>
 GGPG BRI>
 Glu Pro Lys Ser Cys Asp>
 _d_FC TAG_d_d_>

 730 740 750 760
* * * * *
AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT GAA CTC CTG GGG
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly>
_d_d_d_d_d_d_FC TAG_d_d_d_d_d_d_>

 770 780 790 800 810
* * * * *
GGA CCG TCA GTC TTC CTC CCC CCA AAA CCC AAG GAC ACC CTC
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu>
_d_d_d_d_d_d_FC TAG_d_d_d_d_d_d_>

1270 1280 1290 1300

* * * * *

GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG GAC AAG AGC AGG
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg>
_d_d_d_d_d_d_FC TAG_d_d_d_d_d_d_d_d>

1310 1320 1330 1340 1350

* * * * *

TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT
Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala>
_d_d_d_d_d_d_FC TAG_d_d_d_d_d_d_d_d>

1360 1370 1380 1390

* * * * *

CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly>
_d_d_d_d_d_d_FC TAG_d_d_d_d_d_d_d_d>

1400 1410 1420 1430 1440

* * * * *

AAA GGC GGT GGC GGT TCT GGC GCG CCT AGA GAC TGT GCT GAA GTA
Lys>
____>

Gly Gly Gly Gly Ser Gly Ala Pro>
_e_GGGGSGAP BRIDGE_e_e>

Arg Asp Cys Ala Glu Val>
_ANG2 FIBRINOGEN-____>

1450 1460 1470 1480

* * * * *

TTC AAA TCA GGA CAC ACC ACA AAT GGC ATC TAC ACG TTA ACA TTC
Phe Lys Ser Gly His Thr Thr Asn Gly Ile Tyr Thr Leu Thr Phe>
_f_f_f_ANG2 FIBRINOGEN-LIKE DOMAIN_f_f_f_f_f_f>

1490 1500 1510 1520 1530

* * * * *

CCT AAT TCT ACA GAA GAG ATC AAG GCC TAC TGT GAC ATG GAA GCT
Pro Asn Ser Thr Glu Glu Ile Lys Ala Tyr Cys Asp Met Glu Ala>
_f_f_f_ANG2 FIBRINOGEN-LIKE DOMAIN_f_f_f_f_f_f>

1540 1550 1560 1570

* * * * *

GGA GGA GGC GGG TGG ACA ATT ATT CAG CGA CGT GAG GAT GGC AGC
Gly Gly Gly Gly Trp Thr Thr Ile Ile Gln Arg Arg Glu Asp Gly Ser>
_f_f_f_ANG2 FIBRINOGEN-LIKE DOMAIN_f_f_f_f_f_f>

1580 1590 1600 1610 1620

* * * * *

GTT GAT TTT CAG AGG ACT TGG AAA GAA TAT AAA GTG GGA TTT GGT
Val Asp Phe Gln Arg Thr Trp Lys Glu Tyr Lys Val Gly Phe Gly>
_f_f_f_ANG2 FIBRINOGEN-LIKE DOMAIN_f_f_f_f_f_f>

1630 1640 1650 1660

* * * * *

AAC CCT TCA GGA GAA TAT TGG CTG GGA AAT GAG TTT GTT TCG CAA
Asn Pro Ser Gly Glu Tyr Trp Leu Gly Asn Glu Phe Val Ser Gln>
_f_f_f_ANG2 FIBRINOGEN-LIKE DOMAIN_f_f_f_f_f_f>

20/42
Figure 4E

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1670      1680      1690      1700      1710
*          *          *          *          *
CTG ACT AAT CAG CAA CGC TAT GTG CTT AAA ATA CAC CTT AAA GAC
Leu Thr Asn Gln Gln Arg Tyr Val Leu Lys Ile His Leu Lys Asp>
__f__f__f__ANG2 FIBRINOGEN-LIKE DOMAIN_f__f__f__f__>

      1720      1730      1740      1750
*          *          *          *          *
TGG GAA GGG AAT GAG GCT TAC TCA TTG TAT GAA CAT TTC TAT CTC
Trp Glu Gly Asn Glu Ala Tyr Ser Leu Tyr Glu His Phe Tyr Leu>
__f__f__f__ANG2 FIBRINOGEN-LIKE DOMAIN_f__f__f__f__>

1760      1770      1780      1790      1800
*          *          *          *          *
TCA AGT GAA GAA CTC AAT TAT AGG ATT CAC CTT AAA GGA CTT ACA
Ser Ser Glu Glu Leu Asn Tyr Arg Ile His Leu Lys Gly Leu Thr>
__f__f__f__ANG2 FIBRINOGEN-LIKE DOMAIN_f__f__f__f__>

      1810      1820      1830      1840
*          *          *          *          *
GGG ACA GCC GGC AAA ATA AGC AGC ATC AGC CAA CCA GGA AAT GAT
Gly Thr Ala Gly Lys Ile Ser Ser Ile Ser Gln Pro Gly Asn Asp>
__f__f__f__ANG2 FIBRINOGEN-LIKE DOMAIN_f__f__f__f__>

1850      1860      1870      1880      1890
*          *          *          *          *
TTT AGC ACA AAG GAT GGA GAC AAC GAC AAA TGT ATT TGC AAA TGT
Phe Ser Thr Lys Asp Gly Asp Asn Asp Lys Cys Ile Cys Lys Cys>
__f__f__f__ANG2 FIBRINOGEN-LIKE DOMAIN_f__f__f__f__>

      1900      1910      1920      1930
*          *          *          *          *
TCA CAA ATG CTA ACA GGA GGC TGG TGG TTT GAT GCA TGT GGT CCT
Ser Gln Met Leu Thr Gly Gly Trp Trp Phe Asp Ala Cys Gly Pro>
__f__f__f__ANG2 FIBRINOGEN-LIKE DOMAIN_f__f__f__f__>

1940      1950      1960      1970      1980
*          *          *          *          *
TCC AAC TTG AAC GGA ATG TAC TAT CCA CAG AGG CAG AAC ACA AAT
Ser Asn Leu Asn Gly Met Tyr Tyr Pro Gln Arg Gln Asn Thr Asn>
__f__f__f__ANG2 FIBRINOGEN-LIKE DOMAIN_f__f__f__f__>

      1990      2000      2010      2020
*          *          *          *          *
AAG TTC AAC GGC ATT AAA TGG TAC TAC TGG AAA GGC TCA GGC TAT
Lys Phe Asn Gly Ile Lys Trp Tyr Tyr Trp Lys Gly Ser Gly Tyr>
__f__f__f__ANG2 FIBRINOGEN-LIKE DOMAIN_f__f__f__f__>

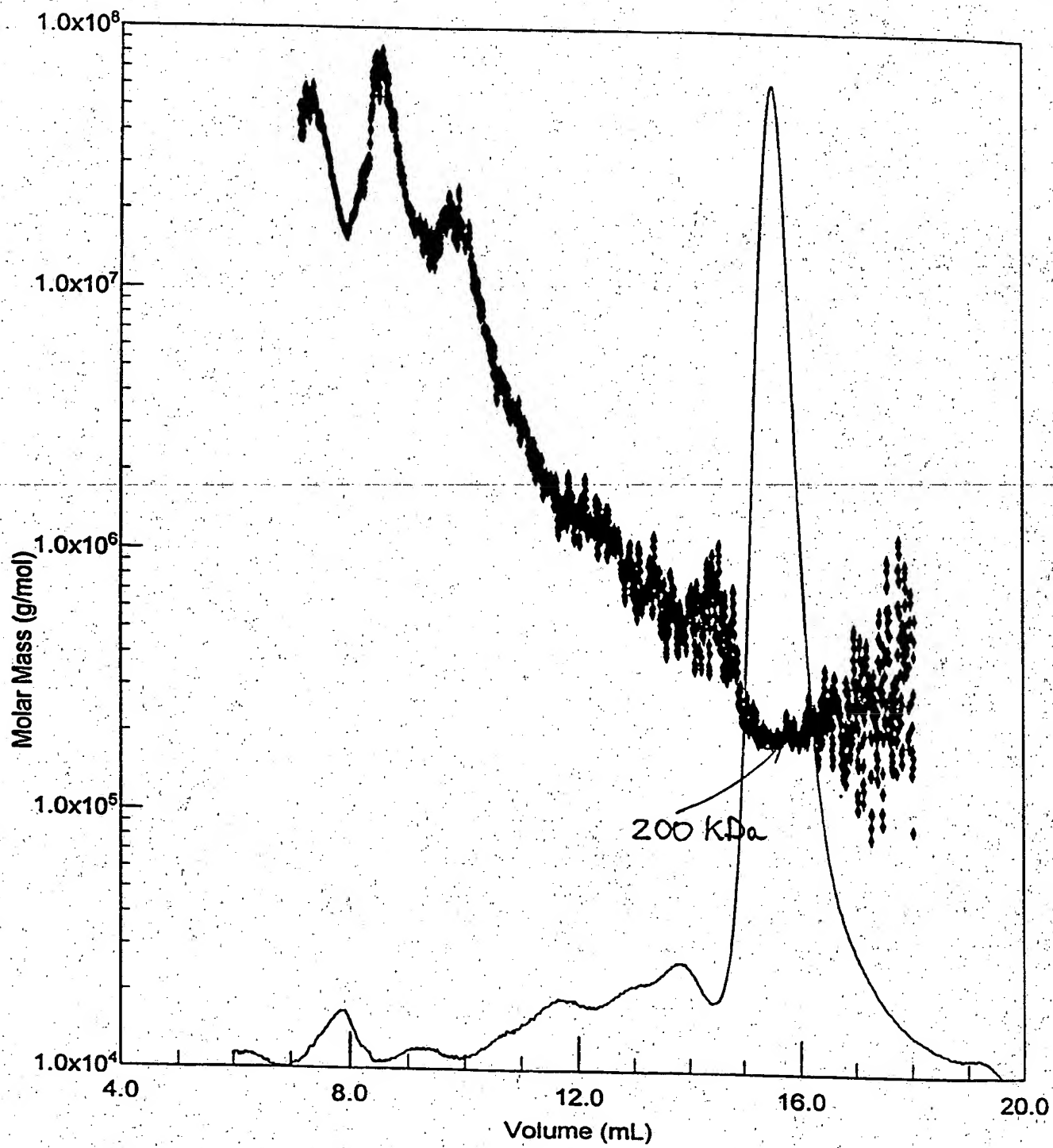
2030      2040      2050      2060      2070
*          *          *          *          *
TCG CTC AAG GCC ACA ACC ATG ATG ATC CGA CCA GCA GAT TTC TGA
Ser Leu Lys Ala Thr Thr Met Met Ile Arg Pro Ala Asp Phe>
__f__f__f__ANG2 FIBRINOGEN-LIKE DOMAIN__f__f__f__f__>

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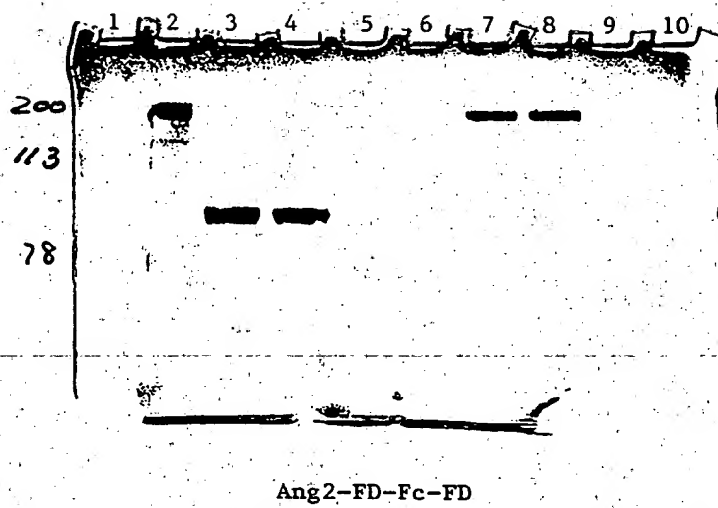
22/42

Figure 6
Molar Mass vs. Volume



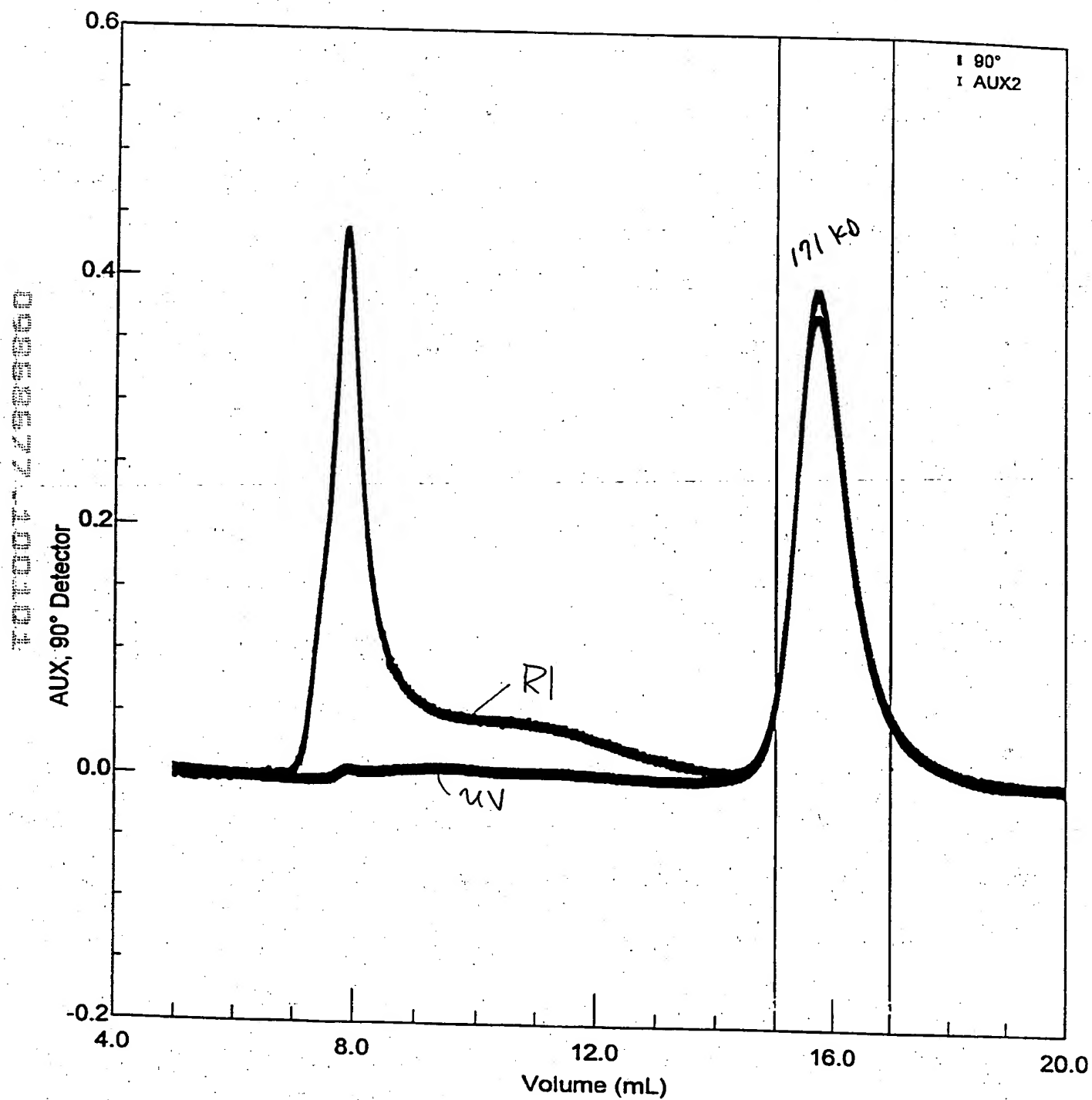
23/42

Figure 7



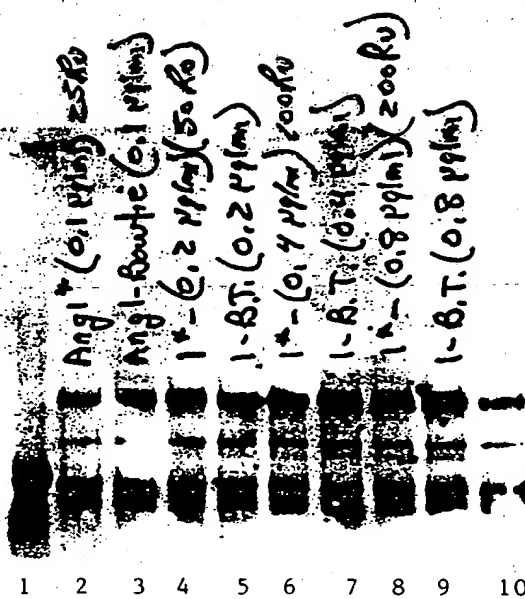
24/42

Figure 8



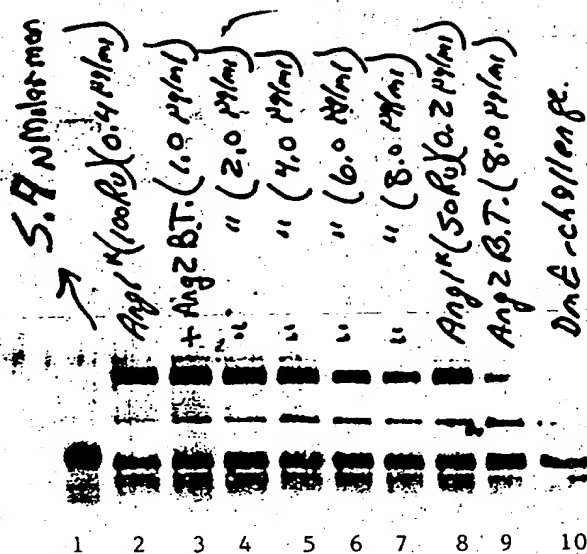
25/42

Figure 9



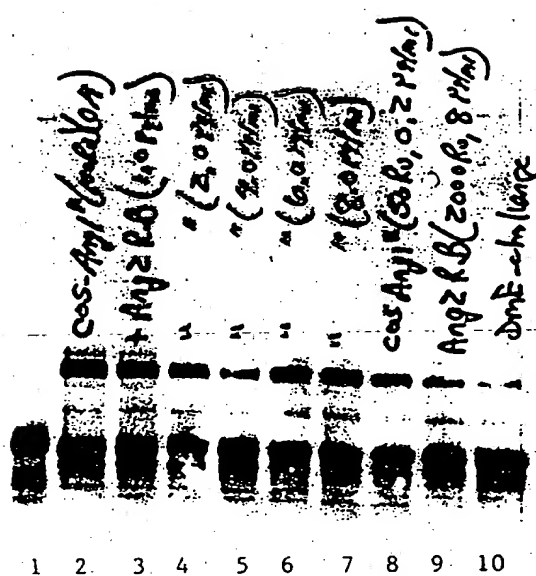
26/42

Figure 10



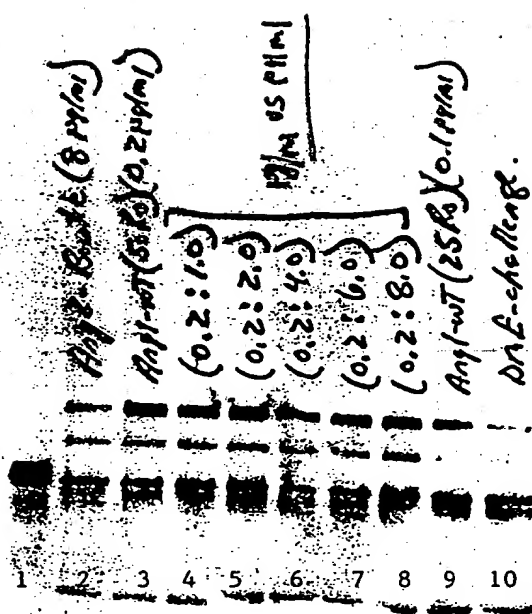
27/42

Figure 11



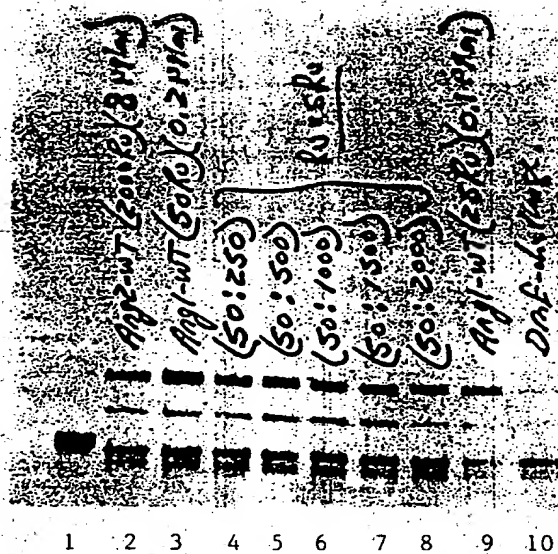
28/42

Figure 12



29/42

Figure 13



30/42

Figure 14A

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      10      20      30      40
      *      *      *      *
ATG GCT CGG CCT GGG CAG CGT TGG CTC GGC AAG TGG CTT GTG GCG
Met Ala Arg Pro Gly Gln Arg Trp Leu Gly Lys Trp Leu Val Ala>
__a__a__ELK-L ECTODOMAIN 1 (WITH SIGNAL PEPTIDE)__a__a__>

      50      60      70      80      90
      *      *      *      *      *
ATG GTC GTG TGG GCG CTG TGC CGG CTC GCC ACA CCG CTG GCC AAG
Met Val Val Trp Ala Leu Cys Arg Leu Ala Thr Pro Leu Ala Lys>
__a__a__ELK-L ECTODOMAIN 1 (WITH SIGNAL PEPTIDE)__a__a__>

     100     110     120     130
      *      *      *      *      *
AAC CTG GAG CCC GTA TCC TGG AGC TCC CTC AAC CCC AAG TTC CTG
Asn Leu Glu Pro Val Ser Trp Ser Ser Leu Asn Pro Lys Phe Leu>
__a__a__ELK-L ECTODOMAIN 1 (WITH SIGNAL PEPTIDE)__a__a__>

     140     150     160     170     180
      *      *      *      *      *
AGT GGG AAG GGC TTG GTG ATC TAT CCG AAA ATT GGA GAC AAG CTG
Ser Gly Lys Gly Leu Val Ile Tyr Pro Lys Ile Gly Asp Lys Leu>
__a__a__ELK-L ECTODOMAIN 1 (WITH SIGNAL PEPTIDE)__a__a__>

     190     200     210     220
      *      *      *      *      *
GAC ATC ATC TGC CCC CGA GCA GAA GCA GGG CGG CCC TAT GAG TAC
Asp Ile Ile Cys Pro Arg Ala Glu Ala Gly Arg Pro Tyr Glu Tyr>
__a__a__ELK-L ECTODOMAIN 1 (WITH SIGNAL PEPTIDE)__a__a__>

     230     240     250     260     270
      *      *      *      *      *
TAC AAG CTG TAC CTG GTG CGG CCT GAG CAG GCA GCT GCC TGT AGC
Tyr Lys Leu Tyr Leu Val Arg Pro Glu Gln Ala Ala Ala Cys Ser>
__a__a__ELK-L ECTODOMAIN 1 (WITH SIGNAL PEPTIDE)__a__a__>

     280     290     300     310
      *      *      *      *      *
ACA GTT CTC GAC CCC AAC GTG TTG GTC ACC TGC AAT AGG CCA GAG
Thr Val Leu Asp Pro Asn Val Leu Val Thr Cys Asn Arg Pro Glu>
__a__a__ELK-L ECTODOMAIN 1 (WITH SIGNAL PEPTIDE)__a__a__>

     320     330     340     350     360
      *      *      *      *      *
CAG GAA ATA CGC TTT ACC ATC AAG TTC CAG GAG TTC AGC CCC AAC
Gln Glu Ile Arg Phe Thr Ile Lys Phe Gln Glu Phe Ser Pro Asn>
__a__a__ELK-L ECTODOMAIN 1 (WITH SIGNAL PEPTIDE)__a__a__>

     370     380     390     400
      *      *      *      *      *
TAC ATG GGC CTG GAG TTC AAG AAG CAC CAT GAT TAC TAC ATT ACC
Tyr Met Gly Leu Glu Phe Lys Lys His His Asp Tyr Tyr Ile Thr>
__a__a__ELK-L ECTODOMAIN 1 (WITH SIGNAL PEPTIDE)__a__a__>

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31/42

Figure 14B

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410      420      430      440      450
*        *        *        *        *
TCA ACA TCC AAT GGA AGC CTG GAG GGG CTG GAA AAC CGG GAG GGC
Ser Thr Ser Asn Gly Ser Leu Glu Gly Leu Glu Asn Arg Glu Gly>
__a__a__a__ELK-L ECTODOMAIN 1 (WITH SIGNAL PEPTIDE)__a__a__a__>

      460      470      480      490
*        *        *        *        *
GGT GTG TGC CGC ACA CGC ACC ATG AAG ATC ATC ATG AAG GTT GGG
Gly Val Cys Arg Thr Arg Thr Met Lys Ile Ile Met Lys Val Gly>
__a__a__a__ELK-L ECTODOMAIN 1 (WITH SIGNAL PEPTIDE)__a__a__a__>

500      510      520      530      540
*        *        *        *        *
CAA GAT CCC AAT GCT GTG ACG CCT GAG CAG CTG ACT ACC AGC AGG
Gln Asp Pro Asn Ala Val Thr Pro Glu Gln Leu Thr Thr Ser Arg>
__a__a__a__ELK-L ECTODOMAIN 1 (WITH SIGNAL PEPTIDE)__a__a__a__>

      550      560      570      580
*        *        *        *        *
CCC AGC AAG GAG GCA GAC AAC ACT GTC AAG ATG GCC ACA CAG GCC
Pro Ser Lys Glu Ala Asp Asn Thr Val Lys Met Ala Thr Gln Ala>
__a__a__a__ELK-L ECTODOMAIN 1 (WITH SIGNAL PEPTIDE)__a__a__a__>

590      600      610      620      630
*        *        *        *        *
CCT GGT AGT CGG GGC TCC CTG GGT GAC TCT GAT GGC AAG CAT GAG
Pro Gly Ser Arg Gly Ser Leu Gly Asp Ser Asp Gly Lys His Glu>
__a__a__a__ELK-L ECTODOMAIN 1 (WITH SIGNAL PEPTIDE)__a__a__a__>

      640      650      660      670
*        *        *        *        *
ACT GTG AAC CAG GAA GAG AAG AGT GGC CCA GGT GCA AGT GGG GGC
Thr Val Asn Gln Glu Glu Lys Ser Gly Pro Gly Ala Ser Gly>
__a__a__a__ELK-L ECTODOMAIN 1 (WITH SIGNAL PEPTIDE)__a__a__a__>

680      690      700      710      720
*        *        *        *        *
AGC AGC GGG GAC CCT GAT GGC TTC TTC AAC TCC AAG GGC CCG GGT
Ser Ser Gly Asp Pro Asp Gly Phe Phe Asn Ser Lys>
__ELK-L ECTODOMAIN 1 (WITH SIGNAL PEPTIDE)____>
                                     Gly Pro Gly>
                                     __b__b__>

      730      740      750      760
*        *        *        *        *
AAG AAC CTG GAG CCC GTA TCC TGG AGC TCC CTC AAC CCC AAG TTC
Lys Asn Leu Glu Pro Val Ser Trp Ser Ser Leu Asn Pro Lys Phe>
__c__c__c__ELK-L ECTODOMAIN 2 (NO SIGNAL)__c__c__c__>

770      780      790      800      810
*        *        *        *        *
CTG AGT GGG AAG GGC TTG GTG ATC TAT CCG AAA ATT GGA GAC AAG
Leu Ser Gly Lys Gly Leu Val Ile Tyr Pro Lys Ile Gly Asp Lys>
__c__c__c__ELK-L ECTODOMAIN 2 (NO SIGNAL)__c__c__c__>

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33/42
Figure 14D

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      1270      1280      1290      1300
      *      *      *      *
GAG ACT GTG AAC CAG GAA GAG AAG AGT GGC CCA GGT GCA AGT GGG
Glu Thr Val Asn Gln Glu Glu Lys Ser Gly Pro Gly Ala Ser Gly>
__c__c__c__ELK-L ECTODOMAIN 2 (NO SIGNAL)__c__c__c__>

      1310      1320      1330      1340      1350
      *      *      *      *      *
GGC AGC AGC GGG GAC CCT GAT GGC TTC TTC AAC TCC AAA GGC CCG
Gly Ser Ser Gly Asp Pro Asp Gly Phe Phe Asn Ser Lys>
__c__c__c__ELK-L ECTODOMAIN 2 (NO SIGNAL)__c__c__c__>
                                     Gly Pro>
                                     __d__>

      1360      1370      1380      1390
      *      *      *      *
GGC GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC
Gly>
__>
      Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys>
      __e__e__e__e__HUMAN IGG1 FC TAG__e__e__e__e__>

      1400      1410      1420      1430      1440
      *      *      *      *      *
CCA GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC
Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro>
__e__e__e__e__HUMAN IGG1 FC TAG__e__e__e__e__>

      1450      1460      1470      1480
      *      *      *      *
CCA AAA CCC AAG GAC ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val>
__e__e__e__e__HUMAN IGG1 FC TAG__e__e__e__e__>

      1490      1500      1510      1520      1530
      *      *      *      *      *
ACA TGC GTG GTG GTG GAC GTG AGC CAC GAA GAC CCT GAG GTC AAG
Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys>
__e__e__e__e__HUMAN IGG1 FC TAG__e__e__e__e__>

      1540      1550      1560      1570
      *      *      *      *
TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT GCC AAG ACA
Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr>
__e__e__e__e__HUMAN IGG1 FC TAG__e__e__e__e__>

      1580      1590      1600      1610      1620
      *      *      *      *      *
AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser>
__e__e__e__e__HUMAN IGG1 FC TAG__e__e__e__e__>

      1630      1640      1650      1660
      *      *      *      *
GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC
Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr>
__e__e__e__e__HUMAN IGG1 FC TAG__e__e__e__e__>

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1670	1680	1690	1700	1710
AAG TGC AAG GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA				
Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys>				
_e_e_e_e_e_HUMAN IGG1 FC TAG_e_e_e_e_e_>				
1720	1730	1740	1750	
ACC ATC TCC AAA GCC AAA GGG CAG CCC CGA GAA CCA CAG GTG TAC				
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr>				
_e_e_e_e_e_HUMAN IGG1 FC TAG_e_e_e_e_e_>				
1760	1770	1780	1790	1800
ACC CTG CCC CCA TCC CGG GAT GAG CTG ACC AAG AAC CAG GTC AGC				
Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser>				
_e_e_e_e_e_HUMAN IGG1 FC TAG_e_e_e_e_e_>				
1810	1820	1830	1840	
CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC ATC GCC GTG				
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val>				
_e_e_e_e_e_HUMAN IGG1 FC TAG_e_e_e_e_e_>				
1850	1860	1870	1880	1890
GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG				
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr>				
_e_e_e_e_e_HUMAN IGG1 FC TAG_e_e_e_e_e_>				
1900	1910	1920	1930	
CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG				
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys>				
_e_e_e_e_e_HUMAN IGG1 FC TAG_e_e_e_e_e_>				
1940	1950	1960	1970	1980
CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA				
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser>				
_e_e_e_e_e_HUMAN IGG1 FC TAG_e_e_e_e_e_>				
1990	2000	2010	2020	
TGC TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC ACG CAG AAG				
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys>				
_e_e_e_e_e_HUMAN IGG1 FC TAG_e_e_e_e_e_>				
2030	2040	2050		
AGC CTC TCC CTG TCT CCG GGT AAA TGA				
Ser Leu Ser Leu Ser Pro Gly Lys ***>				
_e_e_e_e_e_HUMAN IGG1 FC TAG_e_e_e_e_e_>				

35/42
Figure 15A

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      10      20      30      40
      *      *      *      *
ATG GCC ATG GCC CGG TCC AGG AGG GAC TCT GTG TGG AAG TAC TGT
Met Ala Met Ala Arg Ser Arg Arg Asp Ser Val Trp Lys Tyr Cys>
__a__EPHRIN-B2  ECTO DOMAIN 1 (WITH SIGNAL PEPTIDE)__a__>

      50      60      70      80      90
      *      *      *      *      *
TGG GGA CTT TTG ATG GTT TTG TGC AGA ACT GCG ATC TCC AGA TCG
Trp Gly Leu Leu Met Val Leu Cys Arg Thr Ala Ile Ser Arg Ser>
__a__EPHRIN-B2  ECTO DOMAIN 1 (WITH SIGNAL PEPTIDE)__a__>

     100     110     120     130
      *      *      *      *      *
ATA GTT TTA GAG CCT ATC TAC TGG AAT TCC TCG AAC TCC AAA TTT
Ile Val Leu Glu Pro Ile Tyr Trp Asn Ser Ser Asn Ser Lys Phe>
__a__EPHRIN-B2  ECTO DOMAIN 1 (WITH SIGNAL PEPTIDE)__a__>

     140     150     160     170     180
      *      *      *      *      *
CTA CCC GGA CAA GGC CTG GTA CTA TAC CCA CAG ATA GGA GAC AAA
Leu Pro Gly Gln Gly Leu Val Leu Tyr Pro Gln Ile Gly Asp Lys>
__a__EPHRIN-B2  ECTO DOMAIN 1 (WITH SIGNAL PEPTIDE)__a__>

     190     200     210     220
      *      *      *      *      *
TTG GAT ATT ATT TGC CCC AAA GTG GAC TCT AAA ACT GTT GGC CAG
Leu Asp Ile Ile Cys Pro Lys Val Asp Ser Lys Thr Val Gly Gln>
__a__EPHRIN-B2  ECTO DOMAIN 1 (WITH SIGNAL PEPTIDE)__a__>

     230     240     250     260     270
      *      *      *      *      *
TAT GAA TAT TAT AAA GTT TAT ATG GTT GAT AAA GAC CAA GCA GAC
Tyr Glu Tyr Tyr Lys Val Tyr Met Val Asp Lys Asp Gln Ala Asp>
__a__EPHRIN-B2  ECTO DOMAIN 1 (WITH SIGNAL PEPTIDE)__a__>

     280     290     300     310
      *      *      *      *      *
AGA TGC ACA ATT AAG AAG GAG AAT ACC CCG CTG CTC AAC TGT GCC
Arg Cys Thr Ile Lys Lys Glu Asn Thr Pro Leu Leu Asn Cys Ala>
__a__EPHRIN-B2  ECTO DOMAIN 1 (WITH SIGNAL PEPTIDE)__a__>

     320     330     340     350     360
      *      *      *      *      *
AGA CCA GAC CAA GAT GTG AAA TTC ACC ATC AAG TTT CAA GAA TTC
Arg Pro Asp Gln Asp Val Lys Phe Thr Ile Lys Phe Gln Glu Phe>
__a__EPHRIN-B2  ECTO DOMAIN 1 (WITH SIGNAL PEPTIDE)__a__>

     370     380     390     400
      *      *      *      *      *
AGC CCT AAC CTC TGG GGT CTA GAA TTT CAG AAG AAC AAA GAT TAC
Ser Pro Asn Leu Trp Gly Leu Glu Phe Gln Lys Asn Lys Asp Tyr>
__a__EPHRIN-B2  ECTO DOMAIN 1 (WITH SIGNAL PEPTIDE)__a__>

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36/42
Figure 15B

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410      420      430      440      450
*      *      *      *      *
TAC ATT ATA TCT ACA TCA AAT GGG TCT TTG GAG GGC CTG GAT AAC
Tyr Ile Ile Ser Thr Ser Asn Gly Ser Leu Glu Gly Leu Asp Asn>
__a__EPHRIN-B2  ECTO DOMAIN 1 (WITH SIGNAL PEPTIDE) __a__>

      460      470      480      490
*      *      *      *      *
CAG GAG GGA GGG GTG TGC CAG ACA AGA GCC ATG AAG ATC CTC ATG
Gln Glu Gly Gly Val Cys Gln Thr Arg Ala Met Lys Ile Leu Met>
__a__EPHRIN-B2  ECTO DOMAIN 1 (WITH SIGNAL PEPTIDE) __a__>

500      510      520      530      540
*      *      *      *      *
AAA GTT GGA CAA GAT GCA AGT TCT GCT GGA TCA GCC AGG AAT CAC
Lys Val Gly Gln Asp Ala Ser Ser Ala Gly Ser Ala Arg Asn His>
__a__EPHRIN-B2  ECTO DOMAIN 1 (WITH SIGNAL PEPTIDE) __a__>

      550      560      570      580
*      *      *      *      *
GGT CCA ACA AGA CGT CCA GAG CTA GAA GCT GGT ACA AAT GGG AGA
Gly Pro Thr Arg Arg Pro Glu Leu Glu Ala Gly Thr Asn Gly Arg>
__a__EPHRIN-B2  ECTO DOMAIN 1 (WITH SIGNAL PEPTIDE) __a__>

590      600      610      620      630
*      *      *      *      *
AGT TCA ACA ACA AGT CCC TTT GTG AAG CCA AAT CCA GGT TCT AGC
Ser Ser Thr Thr Ser Pro Phe Val Lys Pro Asn Pro Gly Ser Ser>
__a__EPHRIN-B2  ECTO DOMAIN 1 (WITH SIGNAL PEPTIDE) __a__>

      640      650      660      670
*      *      *      *      *
ACC GAT GGC AAC AGC GCG GGG CAT TCC GGG AAC AAT CTC CTG GGG
Thr Asp Gly Asn Ser Ala Gly His Ser Gly Asn Asn Leu Leu Gly>
__a__EPHRIN-B2  ECTO DOMAIN 1 (WITH SIGNAL PEPTIDE) __a__>

680      690      700      710      720
*      *      *      *      *
GGC CCG GGA ATA GTT TTA GAG CCT ATC TAC TGG AAT TCC TCG AAC
Gly Pro Gly>
__b__b__>
Ile Val Leu Glu Pro Ile Tyr Trp Asn Ser Ser Asn>
__EPHRIN-B2  ECTO DOMAIN 2 ( WITHOUT SIGNA__>

      730      740      750      760
*      *      *      *      *
TCC AAA TTT CTA CCC GGA CAA GGC CTG GTA CTA TAC CCA CAG ATA
Ser Lys Phe Leu Pro Gly Gln Gly Leu Val Leu Tyr Pro Gln Ile>
__EPHRIN-B2  ECTO DOMAIN 2 ( WITHOUT SIGNAL PEPTIDE) __e__>

770      780      790      800      810
*      *      *      *      *
GGA GAC AAA TTG GAT ATT ATT TGC CCC AAA GTG GAC TCT AAA ACT
Gly Asp Lys Leu Asp Ile Ile Cys Pro Lys Val Asp Ser Lys Thr>
__EPHRIN-B2  ECTO DOMAIN 2 ( WITHOUT SIGNAL PEPTIDE) __e__>

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37/42
Figure 15C

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      820      830      840      850
      *      *      *      *
GTT GGC CAG TAT GAA TAT TAT AAA GTT TAT ATG GTT GAT AAA GAC
Val Gly Gln Tyr Glu Tyr Tyr Lys Val Tyr Met Val Asp Lys Asp>
____EPHRIN-B2 ECTO DOMAIN 2 ( WITHOUT SIGNAL PEPTIDE)_e____>

      860      870      880      890      900
      *      *      *      *      *
CAA GCA GAC AGA TGC ACA ATT AAG AAG GAG AAT ACC CCG CTG CTC
Gln Ala Asp Arg Cys Thr Ile Lys Lys Glu Asn Thr Pro Leu Leu>
____EPHRIN-B2 ECTO DOMAIN 2 ( WITHOUT SIGNAL PEPTIDE)_e____>

      910      920      930      940
      *      *      *      *      *
AAC TGT GCC AGA CCA GAC CAA GAT GTG AAA TTC ACC ATC AAG TTT
Asn Cys Ala Arg Pro Asp Gln Asp Val Lys Phe Thr Ile Lys Phe>
____EPHRIN-B2 ECTO DOMAIN 2 ( WITHOUT SIGNAL PEPTIDE)_e____>

      950      960      970      980      990
      *      *      *      *      *
CAA GAA TTC AGC CCT AAC CTC TGG GGT CTA GAA TTT CAG AAG AAC
Gln Glu Phe Ser Pro Asn Leu Trp Gly Leu Glu Phe Gln Lys Asn>
____EPHRIN-B2 ECTO DOMAIN 2 ( WITHOUT SIGNAL PEPTIDE)_e____>

     1000     1010     1020     1030
      *      *      *      *      *
AAA GAT TAC TAC ATT ATA TCT ACA TCA AAT GGG TCT TTG GAG GGC
Lys Asp Tyr Tyr Ile Ile Ser Thr Ser Asn Gly Ser Leu Glu Gly>
____EPHRIN-B2 ECTO DOMAIN 2 ( WITHOUT SIGNAL PEPTIDE)_e____>

     1040     1050     1060     1070     1080
      *      *      *      *      *
CTG GAT AAC CAG GAG GGA GGG GTG TGC CAG ACA AGA GCC ATG AAG
Leu Asp Asn Gln Glu Gly Gly Val Cys Gln Thr Arg Ala Met Lys>
____EPHRIN-B2 ECTO DOMAIN 2 ( WITHOUT SIGNAL PEPTIDE)_e____>

     1090     1100     1110     1120
      *      *      *      *      *
ATC CTC ATG AAA GTT GGA CAA GAT GCA AGT TCT GCT GGA TCA GCC
Ile Leu Met Lys Val Gly Gln Asp Ala Ser Ser Ala Gly Ser Ala>
____EPHRIN-B2 ECTO DOMAIN 2 ( WITHOUT SIGNAL PEPTIDE)_e____>

     1130     1140     1150     1160     1170
      *      *      *      *      *
AGG AAT CAC GGT CCA ACA AGA CGC CCA GAG CTA GAA GCT GGT ACA
Arg Asn His Gly Pro Thr Arg Arg Pro Glu Leu Glu Ala Gly Thr>
____EPHRIN-B2 ECTO DOMAIN 2 ( WITHOUT SIGNAL PEPTIDE)_e____>

     1180     1190     1200     1210
      *      *      *      *      *
AAT GGG AGA AGT TCA ACA ACA AGT CCC TTT GTG AAG CCA AAT CCA
Asn Gly Arg Ser Ser Thr Thr Ser Pro Phe Val Lys Pro Asn Pro>
____EPHRIN-B2 ECTO DOMAIN 2 ( WITHOUT SIGNAL PEPTIDE)_e____>

     1220     1230     1240     1250     1260
      *      *      *      *      *
GGT TCT AGC ACC GAT GGC AAC AGC GCG GGC CAT TCC GGG AAC AAT
Gly Ser Ser Thr Asp Gly Asn Ser Ala Gly His Ser Gly Asn Asn>
____EPHRIN-B2 ECTO DOMAIN 2 ( WITHOUT SIGNAL PEPTIDE)_e____>

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05866677-100101

38/42
Figure 15D

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1270      1280      1290      1300
*         *         *         *
CTC CTG GGG G GC CCG GGC GAG CCC AAA TCT TGT GAC AAA ACT CAC
      Glu Pro Lys Ser Cys Asp Lys Thr His>
      ____c____HUMAN IGG1 FC TAG____c____>
      Gly Pro Gly>
      _d_d_d_>
Leu Leu Gly Xxx>
____e____e____e_>

1310      1320      1330      1340      1350
*         *         *         *         *
ACA TGC CCA CCG TGC CCA GCA CCT GAA CTC CTG GGG GGA CCG TCA
Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser>
____c____c____c____c____HUMAN IGG1 FC TAG____c____c____c____c____>

1360      1370      1380      1390
*         *         *         *         *
GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC CTC ATG ATC TCC
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser>
____c____c____c____c____HUMAN IGG1 FC TAG____c____c____c____c____>

1400      1410      1420      1430      1440
*         *         *         *         *
CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC GAA
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu>
____c____c____c____c____HUMAN IGG1 FC TAG____c____c____c____c____>

1450      1460      1470      1480
*         *         *         *         *
GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val>
____c____c____c____c____HUMAN IGG1 FC TAG____c____c____c____c____>

1490      1500      1510      1520      1530
*         *         *         *         *
CAT AAT GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr>
____c____c____c____c____HUMAN IGG1 FC TAG____c____c____c____c____>

1540      1550      1560      1570
*         *         *         *         *
TAC CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu>
____c____c____c____c____HUMAN IGG1 FC TAG____c____c____c____c____>

1580      1590      1600      1610      1620
*         *         *         *         *
AAT GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GCC CTC CCA
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro>
____c____c____c____c____HUMAN IGG1 FC TAG____c____c____c____c____>

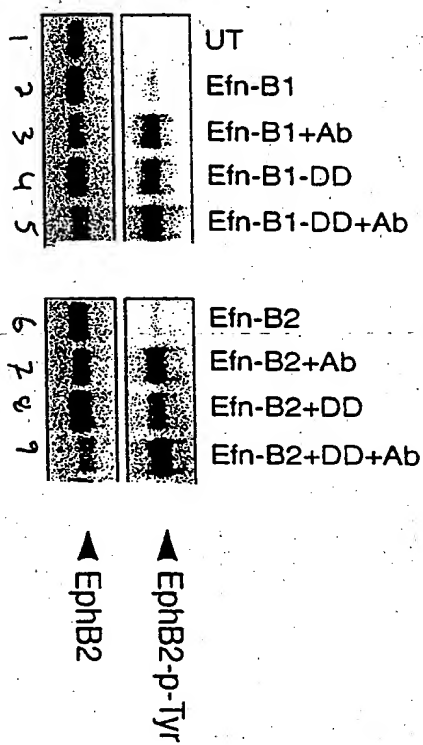
1630      1640      1650      1660
*         *         *         *         *
GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC CGA
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg>
____c____c____c____c____HUMAN IGG1 FC TAG____c____c____c____c____>

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40/42

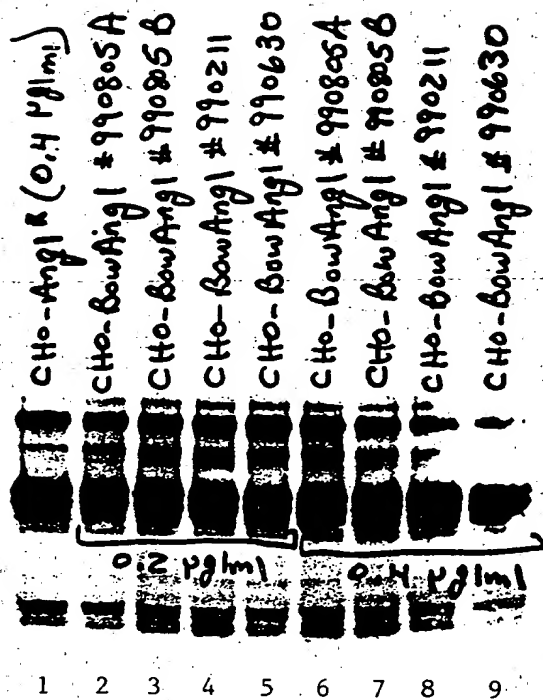
Figure 16



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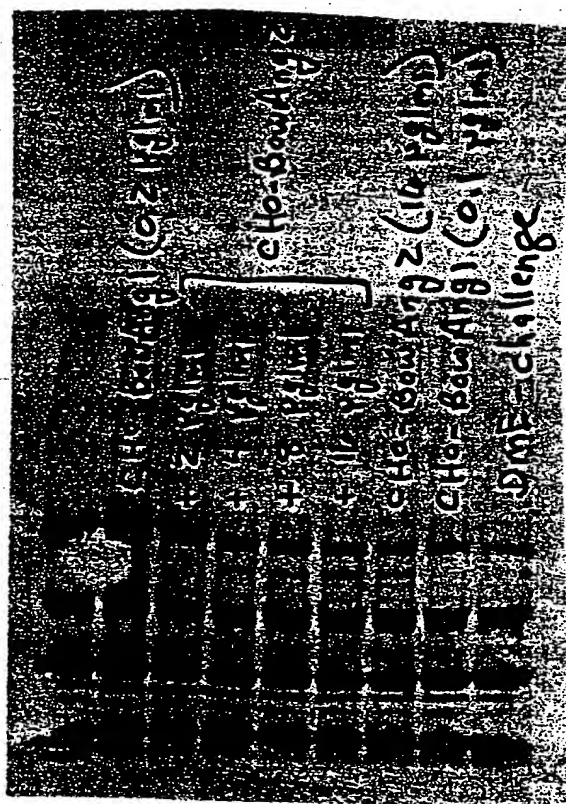
41/42

Figure 17



42/42

Figure 18



1 2 3 4 5 6 7 8 9

09988677-100101